

# CRF Errors Corrected by the STIC Systems Branch

OIPK

7/8/99

Serial Number: 09/339,352

CRF Processing Date: 7/8/99  
 Edited by: [Signature]  
 Verified by: [Signature] (STIC staff)

ENTERED

#2

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/339,352

DATE: 07/08/1999  
TIME: 15:27:55

Input Set: I339352.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

1 <110> APPLICANT: REED-GITOMER, BERENICE Y.  
2 PAK, CHARLES Y.C.  
3 <120> TITLE OF INVENTION: ABSORPTIVE HYPERCALCIURIA LOCUS ON HUMAN CHROMOSOME 1  
4 <130> FILE REFERENCE: UTSD:553  
5 <140> CURRENT APPLICATION NUMBER: US/09/339,352  
6 <141> CURRENT FILING DATE: 1999-06-23  
7 <160> NUMBER OF SEQ ID NOS: 6  
8 <170> SOFTWARE: PatentIn Ver. 2.0  
9 <210> SEQ ID NO 1  
10 <211> LENGTH: 2567  
11 <212> TYPE: DNA  
12 <213> ORGANISM: Human  
13 <400> SEQUENCE: 1  
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16 gtcacctcca acgtcattaa aagaaatctc tctgatccag ctggatagca tgagactttc 180  
17 ccaccaaagt ctggtgagat gtgctgccat cattggcctg accttcacca ctgagttgtt 240  
18 gtttgagatt ctccccgtgt ggaatatgaa gatgatgatc aagacctgg caaccttagt 300  
19 ggaatctaac attttttatt gtttccggaa tggcaaggag cttcaaaagg ccctgaaaca 360  
20 gaatgatccc tcatttgagg tgcactatcg ttccttgtct ctgaagccca gtgaagggat 420  
21 ggatcacggt gaagaggaac agcttcgtga actggagaat gaggtgatcg agtgccacag 480  
22 gattcgattc tgtaacccta tgatgcagaa aacagcctac gagctgtggc tcaaggacca 540  
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24 ccaactgccg ggcagggact tcattcccta tcatcacttc acagtgaata ttcggctcaa 660  
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28 tgcagggact tacttcctca tccacctccc aaaatgaccc tggcaaagga agtgggggtg 900  
29 attcataatt catttaaaaa ctgaagacca acttctcaca gatgtgggga tgctgttcaa 960  
30 ggcatacatg tatttgaatg aaggacagaa gttgctaaaa actctcaaga aggacaaatc 1020  
31 ttggagccag acatttgagt ctgccacctt ttacagcctc aaaggtgagg tctgtttcaa 1080  
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44 ggacatcctg ctttattctg gttttgttta tagaacattt gaagaatggt tgggaattcat 1860

Does Not Comply  
Corrected Diskette Needed

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57 &lt;210&gt; SEQ ID NO 2

58 &lt;211&gt; LENGTH: 372

59 &lt;212&gt; TYPE: PRT

60 &lt;213&gt; ORGANISM: Human

61 &lt;400&gt; SEQUENCE: 2

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64      Lys Thr Leu Lys Lys Asp Lys Ser Trp Ser Gln Thr Phe Glu Ser Ala
65      20              25              30
66      Thr Phe Tyr Ser Leu Lys Gly Glu Val Cys Phe Asn Met Gly Gln Ile
67      35              40              45
68      Val Leu Ala Lys Lys Met Leu Arg Lys Ala Leu Lys Leu Leu Asn Arg
69      50              55              60
70      Ile Phe Pro Tyr Asn Leu Ile Ser Leu Phe Leu His Ile His Val Glu
71      65              70              75              80
72      Lys Asn Arg His Phe His Tyr Val Asn Arg Gln Ala Gln Glu Ser Pro
73      85              90              95
74      Pro Pro Gly Lys Lys Arg Leu Ala Gln Leu Tyr Arg Gln Thr Val Cys
75      100             105             110
76      Leu Ser Leu Leu Trp Arg Ile Tyr Ser Tyr Ser Tyr Leu Phe His Cys
77      115             120             125
78      Lys Tyr Tyr Ala His Leu Ala Val Met Met Gln Met Asn Thr Ala Leu
79      130             135             140
80      Glu Thr Gln Asn Cys Phe Gln Ile Ile Lys Ala Tyr Leu Asp Tyr Ser
81      145             150             155             160
82      Leu Tyr His His Leu Ala Gly Tyr Lys Gly Val Trp Phe Lys Tyr Glu
83      165             170             175
84      Val Met Ala Met Glu His Ile Phe Asn Leu Pro Leu Lys Gly Glu Gly
85      180             185             190
86      Ile Glu Ile Val Ala Tyr Val Ala Glu Thr Leu Val Phe Asn Lys Leu
87      195             200             205
88      Ile Met Gly His Leu Asp Leu Ala Ile Glu Leu Gly Ser Arg Ala Leu
89      210             215             220
90      Gln Met Trp Ala Leu Leu Gln Asn Pro Asn Arg His Tyr Gln Ser Leu
91      225             230             235             240
92      Cys Arg Leu Ser Arg Cys Leu Leu Leu Asn Ser Arg Tyr Pro Gln Leu
93      245             250             255
94      Ile Gln Val Leu Gly Arg Leu Trp Glu Leu Ser Val Thr Gln Glu His

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95          260          265          270
96      Ile Phe Ser Lys Ala Phe Phe Tyr Phe Val Cys Leu Asp Ile Leu Leu
97          275          280          285
98      Tyr Ser Gly Phe Val Tyr Arg Thr Phe Glu Glu Cys Leu Glu Phe Ile
99          290          295          300
100     His Gln Tyr Glu Asn Asn Arg Ile Leu Lys Phe His Ser Gly Leu Leu
101     305          310          315          320
102     Leu Gly Leu Tyr Ser Ser Val Ala Ile Trp Glu Cys Glu Ala Gly Val
103          325          330          335
104     Gly Arg Arg Leu His Thr Ser Arg Asp Pro Gly Met Pro Asp Phe Arg
105          340          345          350
106     Asn Gly Thr Thr Phe Thr Asn Phe Pro Ile Glu Leu Lys Ile Phe Cys
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108     Gln Glu Glu Pro
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112 <212> TYPE: DNA
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116 Primer
117 <400> SEQUENCE: 3
118 gatcgcgccca ctgcactcc 19
119 <210> SEQ ID NO 4
120 <211> LENGTH: 20
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
125 Primer
126 <400> SEQUENCE: 4
127 ggattacagg cgtgagccac 20
128 <210> SEQ ID NO 5
129 <211> LENGTH: 24
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133 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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143 Primer
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RAW SEQUENCE LISTING  
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145 tgattaggag cacagcctca gtgc

24

146

3

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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/339,352

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Line ? Error/Warning

Original Text

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